

# Structure of LCP1 and alignments of domains

FIG. 1A



FIG. 1B

CUB domain	10	20	30	40	50	60	70	80
consensus	1	CGGTLTAS-S--GTITSPNYPNSYPNNLNCVWTISAPPGY-RIELKFTDF-DLESSD-----NCTYDYVEIYDGPSTSSP	70					
LCP1	26	CGHTVLGPes--GTLTsinYPQTPNstVCWEIRVKMGE-RVRIKFGDF-DIEDSD-----SCHFNyLRIYNGIGVSRT	96					
1SPP_B	9	CGRVIKDT-S--GSIINTDRQK-----NLCTWTILMKPDQ-KVRMAIPY--INLA-----CGKEYVEVFDGLL-SGP	68					
gi 1345609	752	CEHKVTSTs---GTITSPNWDkypskECTWAISSTPGH-RVKLTfVEm-DIESqp-----eCAYDHLEVFdGRDaKAP	821					
gi 1168684	484	CGGSFGGTq---GRVATPNPNydnLecVYIEVEIGR-RVELDFIdf-VLEDet-----nCRWDSLSINLGDG--IK	551					
gi 5912464	1766	CGGFLFYA-S--GTFSSPSYPAYpnnAKCWEIEVNSGY-RINLGFsn1-KLEAh-----nCSFDYVEIFdGSlNssL	1835					
gi 2498677	25	CGDTIKIL-Sp-GYLTSpgYPQsyhpsQKCEWLlQAPePYqRIMINFNPhfLEdr-----dCKYDYVEVIDGDNaEGR	96					
gi 2055303	17	vfSAELLT-AhfGNFSSPNYPRsydpnSLTNIRVQHGY-RMSIRfst-fdLEDsyedgigsCVYDYVEITEsn----K	89					
gi 1899042	520	CGGNMPGP-E--GFLNSPAYPdeYgskVCEWITVREGY-QVALEFATf-ETEFdp-----dCAYDYVEIRdGDTkdSP	589					
gi 704441	3	CGHTVLGP-Es-GTLTsinYPQtpnStVCWEIRVKMGE-RVRIKFGDf-DIEDsd-----sCHFNyLRIYNGIGVSRT	73					

	90	100	110	120	130
consensus	71	LLGRFCG-SEL-----PPPISSSSNSMTVTFVSDSSVQKRGFSARYSAV	114		
LCP1	97	EIGKYCGlGLO-----MNHSIESKGNIEITLLFMSGIHVSGRGFLASYSVI	141		
1SPP_B	69	SYGKLCA-GA-----AIVFLSTA-NTMTIKYNRISGNSSSPFLIYFYS	110		
gi 1345609	822	VLGRFCG-SKk-----PEPVLATg-NRMFLRFYSDNSVQRKGFQASHSTE	864		
gi 1168684	552	IDMKMCG-REY-----PAASLVSIGNNMELTLISDRSVtDRGFMADYRAI	595		
gi 5912464	1836	LLGKICN-DT-----RQIFTSSyNRMTIHFRSDISFQNTGFLAWYNSF	1877		
gi 2498677	97	LMGKYCG-KIa-----PPPLVSSg-PYLFIKFVSDYETHGAGFSIRYEVF	139		
gi 2055303	90	TVAKFCG-NYqlfptdapnPSKFIYTSqNEVRVTFVSDYsIsLSGFQAHYAQI	141		
gi 1899042	590	LVGTYCG-Trt-----PPNAISTs-RHLYVKFVSDESMQKGGFSASYLEE	632		
gi 704441	74	EIGKYCG-LG1-----qINHsIESKGNIEITLLFMSGIHVSGRGFLASYSVI	118		

**FIG. 1C**  
**LCCL domain**

		10	20	30	40	50	60	70	80
		.....*	.....*	.....*	.....*	.....*	.....*	.....*	.....*
consensus	1	QAVTCDTKALDLC	--KPVTD	CNRVHCPAGCLLPK	--AKVFGTI	--VYASLSS	ICRAAVHAGVIDNTSGGAVDVVRVGG	72	
LCp1	145	dLITCLDTASNFL	--EPEFSK	--YCPAGCLLPF	--AEISGT	IpHgYRDSSPLCMAGVHAGVVSNTLGGQISVVISKG	215		
gi 12053227	387	QDLDCYTTVAQLCp	feKPATHCPR	IHCPAHCKDEP	sywAPVFGTN	--IYADTSS	ICKTAVHAGVISNESGGDVDMVPVDK	464	
gi 12002311	291	QIVSCEVRLRDQC	--KGTT	CNRYECPAGCLDSK	--AKVIGSV	--HYEMQSS	ICRAAIIHYGIIDND	--GGWVDITRQGR	360
gi 12002311	392	QAVTCETTVEQLCp	fhkPASHCPR	VYCPRNCMQANph	yARVIGTR	--VYSDLSS	ICRAAVHAGVVRNH	--GGYVDVMPVDK	468
gi 12053227	286	QWVRCDTKMKDRC	--KGST	CNRYQCPAGCLNHK	---AKIFGTL	--FYESSSS	ICRAAIIHYGILDDK	--GGLVDITRNGK	355
gi 7387581	26	NAITCFTRGLDLR	--KETED	---VLCPANCPLMQ	---FYVFGDG	--IYASLSS	VCGAAIHRGVITN	--AGGAVRVQITLPG	93
gi 12644458	32	IPVTCFTRGLDIR	--KEKAD	---VLCPGGCSLEE	---FSVFGNI	--VYASVSS	ICGAAVHRGVIGT	--SGGPVRVYSLPG	99
gi 704441	126	LFGHCIQFFWNLS	---SVST	---APAGCLLPF	---AEISGT	IpHgYRDSSPLCMAGVHAGVVSNTLGGQISVVISKG	193		
gi 913964	391	REVDCDSKAVDFL	---DDVGE	PVRIHCPAGCSLTA	---GTVWGTA	--IYHELSS	VCRAAIIHAGKLPN	--SGGAVHVVNNGP	461
gi 6624095	42	PQINCDVKAGKII	---DPEFI	---VKCPAGCQDPK	---YHVYGTD	--VYASYSS	VCGAAVHSGVLDN	--SGGKILVRKVAG	109
		.....*	.....*	.....*	.....*	.....*	.....*	.....*	.....*
		90							
consensus	73	QPYVIGSLANGIQSE	87						
LCp1	216	IPYYESSLANNVTSV	230						
gi 12053227	465	KKTYVGSRLRNGVQSE	479						
gi 12002311	361	KHYFIKSNRNGIQT	375						
gi 12002311	469	RKTYIASFQNGIFSE	483						
gi 12053227	356	VFFVVKSERHGVQSL	370						
gi 7387581	94	QENYPAVHANGIQSQ	108						
gi 12644458	100	RENYSSVDANGIQSQ	114						
gi 704441	194	IPYYESSLANNVTSV	208						
gi 913964	462	YSDFLGSDLNGIKSE	476						
gi 6624095	110	QSGYKGSYSNGVQSL	124						

**FIG. 1D**  
**DSD/FA58C domain**

	10	20	30	40	50	60	70	80
consensus	..... .....* .....* .....* .....* .....* .....* .....*							
LCP1	1 PLGMESG-RIPDSQITASSS	YSAN	WTPENARLNSQGGAGAWSPK	ANDQNQWLQVDLQKPRRVT	62			
1CZT_A	249 tLGMESG-VIADPQITASSV	lewt dhtgQENS	WKPKKARLKKPGPP	WAAF	ATDEYQWLQIDLNKEKKIT	316		
1D7P_M	5 PLGMENG-KIENKQITASSF	KKSwg	dyWEPFRARLNAQGRVNAWQAK	ANNKQWLQVDLQKPRRVT	70			
gi 2547128	7 PLGMESK-AISDAQITASSY	FTNmf	twSPSKARLHLQGRSNARWPK	VNNPKEWLQVDFQTKMKVT	71			
gi 2506380	280 PLGMESG-RIANEQISAST	FSDGr	WTPQOQSRHLGDD	NGWTPN	LDSNKEYLQVDLRLFLTMLT	340		
gi 127058	233 PLGLKNN-SIPDKQITASSS	YKTWglhl	fswNPSYARLDKQGNFNAWVAG	SYGNDQWLQVDLQKPRRVT	300			
gi 2645493	311 PLGLKNN-TIPDSQMSASSS	YKTWnl	rafgWYPHLGRLDNQKINAWTAQ	SNSAKEWLQVDLQKPRRVT	378			
gi 2623894	2035 PLGMASG-HIRDFQITASGQ	YGQ	WAPKLARLHYSGSINAWSTKd	PFS	WIKVDLILAPMIH	2093		
gi 704441	322 PLGMKSG-HIQDYQITASSV	FRTLmndmft	WEPKARLDKQKVNAWTSG	HNDQSQWLQVDLQKPRRVT	389			
	228 TLGMESGgDRGSSNNSITVL	EWTdhtgqens	WKP	KKSQAek	TWTALgafATDEYQWLQIDLNKEKKIT	295		
	90	100	110	120	130	140	150	160
consensus	.....* .....* .....* .....* .....* .....* .....* .....*							
LCP1	63 GVITQGRKDFGSS	QWVTSYKVQYSDDGRTWT	TYKDGd	GKPKIFPGNSDRNT	PVTNDFDPPIVARYIRILPLTWG	137		
1CZT_A	317 GIITGSTMVEHN	YVVSAYRILYSDDGQKWTVYR	EPGvEQDKILFQGNKDYHQ	DVERNFLPPIIARFIRVNPTQWQ	392			
1D7P_M	71 AIITQGCKSLSE	MVVKSYTIHYSEQGV	EWKPYRLKSMVDKIFEGNTNTKG	HVKNFNPPPIISRFIRVPIKTWNQ	146			
gi 2547128	72 GVTTQGVKSLITS	MVKEFLISSQDGHQWTL	FFQN	GKVKVFQGNQDSFT	PVVNCLDPPLLTRYLRIHPQSWVH	145		
gi 2506380	341 AIATQGAISRETQk	gYVVKSYKLEVSTNGEDW	WVYRHG	KNHKIFQANNDATE	VVLNKLHMPLLTRFIRIRPQTWHL	416		
gi 127058	301 GIITQGARNFGSV	QFVASYKVAHSDDGVQWTV	VVEEQ	GSSKVFQGNLDNNS	HKKNIFKFPFMARYVRVLPVSWHN	452		
gi 2645493	379 GIITQGARDFGHI	QYVESYKVAHSDDGVQWTV	VVEEQ	GSSKVFQGNLDNNS	IKHNIFNPPPIIAQYIRLHPHYSI	2169		
gi 2623894	2094 GIMTQGARQKFSS	LYVSQFLIMYSILDGNKWH	SYRGNStGTLMVFFGNVDSSG	HRKNVIDPPIYARFIRILPWSWYG	465			
gi 704441	390 GIITQGAKDFGHV	QFVGSYKLAYSNDGEH	WMVHQDEKqRDKVFQGNFNDT	HRKNVIDPPIYARFIRILPWSWYG	465			
	296 GIITGSTMVSTIcmclPTESCTVMGRNGL	CTESLVVe	QD	KIFQGNKRIITrMVRNNFLPPIIAR	-----	361		
	138 RI 139							
LCP1	393 KI 394							
1CZT_A	147 SI 148							
1D7P_M	146 QI 147							
gi 2547128	417 GI 418							
gi 2506380	377 RI 378							
gi 127058	453 RI 454							
gi 2645493	2170 RS 2171							
gi 2623894	466 RI 467							
gi 704441	362 -L 362							

GenBank accession number: AC091213.8

# Structure of the LCP gene (Chr. 3q12.1)

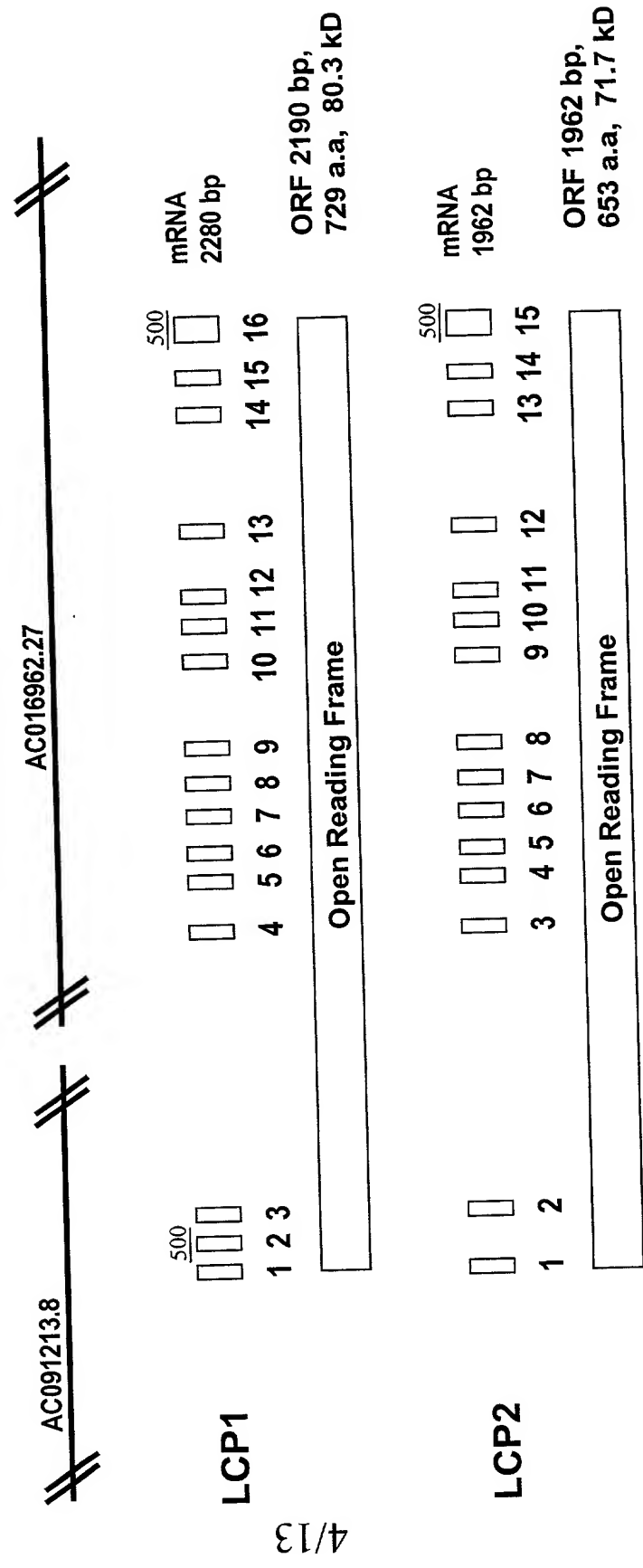


FIG. 2

# LCP1

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

gcgcgcgcgcgcgcctggggcgcgcgtccccctctcccgcgtccctccctccct													52
						M	P	L	F	L	L	L	7
gctccaactcctcctccttctcc						ATG	CCT	CTG	TTC	CTC	CTG	CTC	96
L	L	V	L	L	L	L	L	E	D	A	G	A	20
TTA	CTT	GTC	CTG	CTC	CTG	CTG	CTC	GAG	GAC	GCT	GGA	GCC	135
Q	Q	G	D	G	C	G	H	T	V	L	G	P	33
CAG	CAA	GGT	GAT	GGA	TGT	GGA	CAC	ACT	GTA	CTA	GGC	CCT	174
E	S	G	T	L	T	S	I	N	Y	P	Q	T	46
GAG	AGT	GGA	ACC	CTT	ACA	TCC	ATA	AAC	TAC	CCA	CAG	ACC	213
Y	P	N	S	T	V	C	E	W	E	I	R	V	59
TAT	CCC	AAC	AGC	ACT	GTT	TGT	GAA	TGG	GAG	ATC	CGT	GTA	252
K	M	G	E	R	V	R	I	K	F	G	D	F	72
AAG	ATG	GGA	GAG	AGA	GTT	CGC	ATC	AAA	TTT	GGT	GAC	TTT	291
D	I	E	D	S	D	S	C	H	F	N	Y	L	85
GAC	ATT	GAA	GAT	TCT	GAT	TCT	TGT	CAC	TTT	AAT	TAC	TTG	330
R	I	Y	N	G	I	G	V	S	R	T	E	I	98
AGA	ATT	TAT	AAT	GGA	ATT	GGA	GTC	AGC	AGA	ACT	GAA	ATA	369
G	K	Y	C	G	L	G	L	Q	M	N	H	S	111
GGC	AAA	TAC	TGT	GGT	CTG	GGG	TTG	CAA	ATG	AAC	CAT	TCA	408
I	E	S	K	G	N	E	I	T	L	L	F	M	124
ATT	GAA	TCA	AAA	GGC	AAT	GAA	ATC	ACA	TTG	CTG	TTC	ATG	447
S	G	I	H	V	S	G	R	G	F	L	A	S	137
AGT	GGA	ATC	CAT	GTT	TCT	GGA	CGC	GGA	TTT	TTG	GCC	TCA	486
Y	S	V	I	D	K	Q	D	L	I	T	C	L	150
TAC	TCT	GTT	ATA	GAT	AAA	CAA	GAT	CTA	ATT	ACT	TGT	TTG	525
D	T	A	S	N	F	L	E	P	E	F	S	K	163
GAC	ACT	GCA	TCC	AAT	TTT	TTG	GAA	CCT	GAG	TTC	AGT	AAG	564

**FIG. 3**

Y	C	P	A	G	C	L	L	P	F	A	E	I	176
TAC	TGC	CCA	GCT	GGT	TGT	CTG	CTT	CCT	TTT	GCT	GAG	ATA	603
S	G	T	I	P	H	G	Y	R	D	S	S	P	189
TCT	GGA	ACA	ATT	CCT	CAT	GGA	TAT	AGA	GAT	TCC	TCG	CCA	642
L	C	M	A	G	V	H	A	G	V	V	S	N	202
TTG	TGC	ATG	GCT	GGT	GTG	CAT	GCA	GGA	GTA	GTG	TCA	AAC	681
T	L	G	G	Q	I	S	V	V	I	S	K	G	215
ACG	TTG	GGC	GGC	CAA	ATC	AGT	GTT	GTA	ATT	AGT	AAA	GGT	720
I	P	Y	Y	E	S	S	L	A	N	N	V	T	228
ATT	CCC	TAT	TAT	GAA	AGT	TCT	TTG	GCT	AAC	AAC	GTC	ACA	759
S	V	V	G	H	L	S	T	S	L	F	T	F	241
TCT	GTG	GTG	GGA	CAC	TTA	TCT	ACA	AGT	CTT	TTT	ACA	TTT	798
K	T	S	G	C	Y	G	T	L	G	M	E	S	254
AAG	ACA	AGT	GGA	TGT	TAT	GGA	ACA	CTG	GGG	ATG	GAG	TCT	837
G	V	I	A	D	P	Q	I	T	A	S	S	V	267
GGT	GTG	ATC	GCG	GAT	CCT	CAA	ATA	ACA	GCA	TCA	TCT	GTG	876
L	E	W	T	D	H	T	G	Q	E	N	S	W	280
CTG	GAG	TGG	ACT	GAC	CAC	ACA	GGG	CAA	GAG	AAC	AGT	TGG	915
K	P	K	K	A	R	L	K	K	P	G	P	P	293
AAA	CCC	AAA	AAA	GCC	AGG	CTG	AAA	AAA	CCT	GGA	CCG	CCT	954
W	A	A	F	A	T	D	E	Y	Q	W	L	Q	306
TGG	GCT	GCT	TTT	GCC	ACT	GAT	GAA	TAC	CAG	TGG	TTA	CAA	993
I	D	L	N	K	E	K	K	I	T	G	I	I	319
ATA	GAT	TTG	AAT	AAG	GAA	AAG	AAA	ATA	ACA	GGC	ATT	ATA	1032
T	T	G	S	T	M	V	E	H	N	Y	Y	V	332
ACC	ACT	GGA	TCC	ACC	ATG	GTG	GAG	CAC	AAT	TAC	TAT	GTG	1071
S	A	Y	R	I	L	Y	S	D	D	G	Q	K	345
TCT	GCC	TAC	AGA	ATC	CTG	TAC	AGT	GAT	GAT	GGG	CAG	AAA	1110
W	T	V	Y	R	E	P	G	V	E	Q	D	K	358
TGG	ACT	GTG	TAC	AGA	GAG	CCT	GGT	GTG	GAG	CAA	GAT	AAG	1149
I	F	Q	G	N	K	D	Y	H	Q	D	V	R	371
ATA	TTT	CAA	GGA	AAC	AAA	GAT	TAT	CAC	CAG	GAT	GTG	CGT	1188
N	N	F	L	P	P	I	I	A	R	F	I	R	384
AAT	AAC	TTT	TTG	CCA	CCA	ATT	ATT	GCA	CGT	TTT	ATT	AGA	1227

FIG. 3

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V	N	P	T	Q	W	Q	Q	K	I	A	M	K	397
GTG	AAT	CCT	ACC	CAA	TGG	CAG	CAG	AAA	ATT	GCC	ATG	AAA	1266
M	E	L	L	G	C	Q	F	I	P	K	G	R	410
ATG	GAG	CTG	CTC	GGA	TGT	CAG	TTT	ATT	CCT	AAA	GGT	CGT	1305
P	P	K	L	T	Q	P	P	P	P	R	N	S	423
CCT	CCA	AAA	CTT	ACT	CAA	CCT	CCA	CCT	CCT	CGG	AAC	AGC	1344
N	D	L	K	N	T	T	A	P	P	K	I	A	436
AAT	GAC	CTC	AAA	AAC	ACT	ACA	GCC	CCT	CCA	AAA	ATA	GCC	1383
K	G	R	A	P	K	F	T	Q	P	L	Q	P	449
AAA	GGT	CGT	GCC	CCA	AAA	TTT	ACG	CAA	CCA	CTA	CAA	CCT	1422
R	S	S	N	E	F	P	A	Q	T	E	Q	T	462
CGC	AGT	AGC	AAT	GAA	TTT	CCT	GCA	CAG	ACA	GAA	CAA	ACA	1461
T	A	S	P	D	I	R	N	T	T	V	T	P	475
ACT	GCC	AGT	CCT	GAT	ATC	AGA	AAT	ACT	ACC	GTA	ACT	CCA	1500
N	V	T	K	D	V	A	L	A	A	V	L	V	488
AAT	GTA	ACC	AAA	GAT	GTA	GCG	CTG	GCT	GCA	GTT	CTT	GTC	1539
P	V	L	V	M	V	L	T	T	L	I	L	I	501
CCT	GTG	CTG	GTC	ATG	GTC	CTC	ACT	ACT	CTC	ATT	CTC	ATA	1578
L	V	C	A	W	H	W	R	N	R	K	K	K	514
TTA	GTG	TGT	GCT	TGG	CAC	TGG	AGA	AAC	AGA	AAG	AAA	AAA	1617
T	E	G	T	Y	D	L	P	Y	W	D	R	A	527
ACT	GAA	GGC	ACC	TAT	GAC	TTA	CCT	TAC	TGG	GAC	CGG	GCA	1656
G	W	W	K	G	M	K	Q	F	L	P	A	K	540
GGT	TGG	TGG	AAA	GGA	ATG	AAG	CAG	TTT	CTT	CCT	GCA	AAA	1695
A	V	D	H	E	E	T	P	V	R	Y	S	S	553
GCA	GTG	GAC	CAT	GAG	GAA	ACC	CCA	GTT	CGC	TAT	AGC	AGC	1734
S	E	V	N	H	L	S	P	R	E	V	T	T	566
AGC	GAA	GTT	AAT	CAC	CTG	AGT	CCA	AGA	GAA	GTC	ACC	ACA	1773
V	L	Q	A	D	S	A	E	Y	A	Q	P	L	579
GTG	CTG	CAG	GCT	GAC	TCT	GCA	GAG	TAT	GCT	CAG	CCA	CTG	1812
V	G	G	I	V	G	T	L	H	Q	R	S	T	592
GTA	GGA	GGA	ATT	GTT	GGT	ACA	CTT	CAT	CAA	AGA	TCT	ACC	1851
F	K	P	E	E	G	K	E	A	G	Y	A	D	605
TTT	AAA	CCA	GAA	GAA	GGA	AAA	GAA	GCA	GGC	TAT	GCA	GAC	1890
L	D	P	Y	N	S	P	G	Q	E	V	Y	H	618
CTA	GAT	CCT	TAC	AAC	TCA	CCA	GGG	CAG	GAA	GTT	TAT	CAT	1929

FIG. 3

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A	Y	A	E	P	L	P	I	T	G	P	E	Y	631
GCC	TAT	GCT	GAA	CCA	CTC	CCA	ATT	ACG	GGG	CCT	GAG	TAT	1968
A	T	P	I	I	M	D	M	S	G	H	P	T	644
GCA	ACC	CCA	ATC	ATC	ATG	GAC	ATG	TCA	GGG	CAC	CCC	ACA	2007
T	S	V	G	Q	P	S	T	S	T	F	K	A	657
ACT	TCA	GTT	GGT	CAG	CCC	TCC	ACA	TCC	ACT	TTC	AAG	GCT	2046
T	G	N	Q	P	P	P	L	V	G	T	Y	N	670
ACG	GGG	AAC	CAA	CCT	CCC	CCA	CTA	GTG	GGA	ACT	TAC	AAT	2085
T	L	L	S	R	T	D	S	C	S	S	A	Q	683
ACA	CTT	CTC	TCC	AGG	ACT	GAC	AGC	TGC	TCC	TCA	GCC	CAG	2124
A	Q	Y	D	T	P	K	A	G	K	P	G	L	696
GCC	CAG	TAT	GAT	ACC	CCG	AAA	GCT	GGG	AAG	CCA	GGT	CTA	2163
P	A	P	D	E	L	V	Y	Q	V	P	Q	S	709
CCT	GCC	CCA	GAC	GAA	TTG	GTG	TAC	CAG	GTG	CCA	CAG	AGC	2202
T	Q	E	V	S	G	A	G	R	D	G	E	C	722
ACA	CAA	GAA	GTA	TCA	GGA	GCA	GGA	AGG	GAT	GGG	GAA	TGT	2241
D	V	F	K	E	I	L	*						730
GAT	GTT	TTT	AAA	GAA	ATC	CTT	TGA	agatgatgctgcttt					2280

FIG. 3



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## LCP2

nt: SEQ ID NO: 1113

aa: SEQ ID NO: 1114

M	P	L	F	L	L	L	L	L	V	L	L	L	13
ATG	CCT	CTG	TTC	CTC	CTG	CTC	TTA	CTT	GTC	CTG	CTC	CTG	39
L	L	E	D	A	G	A	Q	Q	G	K	Y	C	26
CTG	CTC	GAG	GAC	GCT	GGA	GCC	CAG	CAA	GGC	AAA	TAC	TGT	78
G	L	G	L	Q	M	N	H	S	I	E	S	K	39
GGT	CTG	GGG	TTG	CAA	ATG	AAC	CAT	TCA	ATT	GAA	TCA	AAA	117
G	N	E	I	T	L	L	F	M	S	G	I	H	52
GGC	AAT	GAA	ATC	ACA	TTG	CTG	TTC	ATG	AGT	GGA	ATC	CAT	156
V	S	G	R	G	F	L	A	S	Y	S	V	I	65
GTT	TCT	GGA	CGC	GGA	TTT	TTG	GCC	TCA	TAC	TCT	GTT	ATA	195
D	K	Q	D	L	I	T	C	L	D	T	A	S	78
GAT	AAA	CAA	GAT	CTA	ATT	ACT	TGT	TTG	GAC	ACT	GCA	TCC	234
N	F	L	E	P	E	F	S	K	Y	C	P	A	91
AAT	TTT	TTG	GAA	CCT	GAG	TTC	AGT	AAG	TAC	TGC	CCA	GCT	273
G	C	L	L	P	F	A	E	I	S	G	T	I	104
GGT	TGT	CTG	CTT	CCT	TTT	GCT	GAG	ATA	TCT	GGA	ACA	ATT	312
P	H	G	Y	R	D	S	S	P	L	C	M	A	117
CCT	CAT	GGA	TAT	AGA	GAT	TCC	TCG	CCA	TTG	TGC	ATG	GCT	351
G	V	H	A	G	V	V	S	N	T	L	G	G	130
GGT	GTG	CAT	GCA	GGA	GTA	GTG	TCA	AAC	ACG	TTG	GGC	GGC	390
Q	I	S	V	V	I	S	K	G	I	P	Y	Y	143
CAA	ATC	AGT	GTT	GTA	ATT	AGT	AAA	GGT	ATT	CCC	TAT	TAT	429
E	S	S	L	A	N	N	V	T	S	V	V	G	156
GAA	AGT	TCT	TTG	GCT	AAC	AAC	GTC	ACA	TCT	GTG	GTG	GGA	468

FIG. 4

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H	L	S	T	S	L	F	T	F	K	T	S	G	169
CAC	TTA	TCT	ACA	AGT	CTT	TTT	ACA	TTT	AAG	ACA	AGT	GGA	507
C	Y	G	T	L	G	M	E	S	G	V	I	A	182
TGT	TAT	GGA	ACA	CTG	GGG	ATG	GAG	TCT	GGT	GTG	ATC	GCG	546
D	P	Q	I	T	A	S	S	V	L	E	W	T	195
GAT	CCT	CAA	ATA	ACA	GCA	TCA	TCT	GTG	CTG	GAG	TGG	ACT	585
D	H	T	G	Q	E	N	S	W	K	P	K	K	208
GAC	CAC	ACA	GGG	CAA	GAG	AAC	AGT	TGG	AAA	CCC	AAA	AAA	624
A	R	L	K	K	P	G	P	P	W	A	A	F	221
GCC	AGG	CTG	AAA	AAA	CCT	GGA	CCG	CCT	TGG	GCT	GCT	TTT	663
A	T	D	E	Y	Q	W	L	Q	I	D	L	N	234
GCC	ACT	GAT	GAA	TAC	CAG	TGG	TTA	CAA	ATA	GAT	TTG	AAT	702
K	E	K	K	I	T	G	I	I	T	T	G	S	247
AAG	GAA	AAG	AAA	ATA	ACA	GGC	ATT	ATA	ACC	ACT	GGA	TCC	741
T	M	V	E	H	N	Y	Y	V	S	A	Y	R	260
ACC	ATG	GTG	GAG	CAC	AAT	TAC	TAT	GTG	TCT	GCC	TAC	AGA	780
I	L	Y	S	D	D	G	Q	K	W	T	V	Y	273
ATC	CTG	TAC	AGT	GAT	GAT	GGG	CAG	AAA	TGG	ACT	GTG	TAC	819
R	E	P	G	V	E	Q	D	K	I	F	Q	G	286
AGA	GAG	CCT	GGT	GTG	GAG	CAA	GAT	AAG	ATA	TTT	CAA	GGA	858
N	K	D	Y	H	Q	D	V	R	N	N	F	L	299
AAC	AAA	GAT	TAT	CAC	CAG	GAT	GTG	CGT	AAT	AAC	TTT	TTG	897
P	P	I	I	A	R	F	I	R	V	N	P	T	312
CCA	CCA	ATT	ATT	GCA	CGT	TTT	ATT	AGA	GTG	AAT	CCT	ACC	936
Q	W	Q	Q	K	I	A	M	K	M	E	L	L	325
CAA	TGG	CAG	CAG	AAA	ATT	GCC	ATG	AAA	ATG	GAG	CTG	CTC	975
G	C	Q	F	I	P	K	G	R	P	P	K	L	338
GGA	TGT	CAG	TTT	ATT	CCT	AAA	GGT	CGT	CCT	CCA	AAA	CTT	1014

FIG. 4

T	Q	P	P	P	P	R	N	S	N	D	L	K	351
ACT	CAA	CCT	CCA	CCT	CCT	CGG	AAC	AGC	AAT	GAC	CTC	AAA	1053
N	T	T	A	P	P	K	I	A	K	G	R	A	364
AAC	ACT	ACA	GCC	CCT	CCA	AAA	ATA	GCC	AAA	GGT	CGT	GCC	1092
P	K	F	T	Q	P	L	Q	P	R	S	S	N	377
CCA	AAA	TTT	ACG	CAA	CCA	CTA	CAA	CCT	CGC	AGT	AGC	AAT	1131
E	F	P	A	Q	T	E	Q	T	T	A	S	P	390
GAA	TTT	CCT	GCA	CAG	ACA	GAA	CAA	ACA	ACT	GCC	AGT	CCT	1170
D	I	R	N	T	T	V	T	P	N	V	T	K	403
GAT	ATC	AGA	AAT	ACT	ACC	GTA	ACT	CCA	AAT	GTA	ACC	AAA	1209
D	V	A	L	A	A	V	L	V	P	V	L	V	416
GAT	GTA	GCG	CTG	GCT	GCA	GTT	CTT	GTC	CCT	GTG	CTG	GTC	1248
M	V	L	T	T	L	I	L	I	L	V	C	A	429
ATG	GTC	CTC	ACT	ACT	CTC	ATT	CTC	ATA	TTA	GTG	TGT	GCT	1287
W	H	W	R	N	R	K	K	K	T	E	G	T	442
TGG	CAC	TGG	AGA	AAC	AGA	AAG	AAA	AAA	ACT	GAA	GGC	ACC	1326
Y	D	L	P	Y	W	D	R	A	G	W	W	K	455
TAT	GAC	TTA	CCT	TAC	TGG	GAC	CGG	GCA	GGT	TGG	TGG	AAA	1365
G	M	K	Q	F	L	P	A	K	A	V	D	H	468
GGA	ATG	AAG	CAG	TTT	CTT	CCT	GCA	AAA	GCA	GTG	GAC	CAT	1404
E	E	T	P	V	R	Y	S	S	S	E	V	N	481
GAG	GAA	ACC	CCA	GTT	CGC	TAT	AGC	AGC	AGC	GAA	GTT	AAT	1443
H	L	S	P	R	E	V	T	T	V	L	Q	A	494
CAC	CTG	AGT	CCA	AGA	GAA	GTC	ACC	ACA	GTG	CTG	CAG	GCT	1482
D	S	A	E	Y	A	Q	P	L	V	G	G	I	507
GAC	TCT	GCA	GAG	TAT	GCT	CAG	CCA	CTG	GTA	GGA	GGA	ATT	1521
V	G	T	L	H	Q	R	S	T	F	K	P	E	520
GTT	GGT	ACA	CTT	CAT	CAA	AGA	TCT	ACC	TTT	AAA	CCA	GAA	1560
E	G	K	E	A	G	Y	A	D	L	D	P	Y	533

FIG. 4

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GAA	GGA	AAA	GAA	GCA	GGC	TAT	GCA	GAC	CTA	GAT	CCT	TAC	1599
N	S	P	G	Q	E	V	Y	H	A	Y	A	E	546
AAC	TCA	CCA	GGG	CAG	GAA	GTT	TAT	CAT	GCC	TAT	GCT	GAA	1638
P	L	P	I	T	G	P	E	Y	A	T	P	I	559
CCA	CTC	CCA	ATT	ACG	GGG	CCT	GAG	TAT	GCA	ACC	CCA	ATC	1677
I	M	D	M	S	G	H	P	T	T	S	V	G	572
ATC	ATG	GAC	ATG	TCA	GGG	CAC	CCC	ACA	ACT	TCA	GTT	GGT	1716
Q	P	S	T	S	T	F	K	A	T	G	N	Q	585
CAG	CCC	TCC	ACA	TCC	ACT	TTC	AAG	GCT	ACG	GGG	AAC	CAA	1755
P	P	P	L	V	G	T	Y	N	T	L	L	S	598
CCT	CCC	CCA	CTA	GTG	GGA	ACT	TAC	AAT	ACA	CTT	CTC	TCC	1794
R	T	D	S	C	S	S	A	Q	A	Q	Y	D	611
AGG	ACT	GAC	AGC	TGC	TCC	TCA	GCC	CAG	GCC	CAG	TAT	GAT	1833
T	P	K	A	G	K	P	G	L	P	A	P	D	624
ACC	CCG	AAA	GCT	GGG	AAG	CCA	GGT	CTA	CCT	GCC	CCA	GAC	1872
E	L	V	Y	Q	V	P	Q	S	T	Q	E	V	637
GAA	TTG	GTG	TAC	CAG	GTG	CCA	CAG	AGC	ACA	CAA	GAA	GTA	1911
S	G	A	G	R	D	G	E	C	D	V	F	K	650
TCA	GGA	GCA	GGA	AGG	GAT	GGG	GAA	TGT	GAT	GTT	TTT	AAA	1950
E	I	L	*										654
GAA	ATC	CTT	TGA										1962

FIG. 4

# Tissue Expression profile of LCP

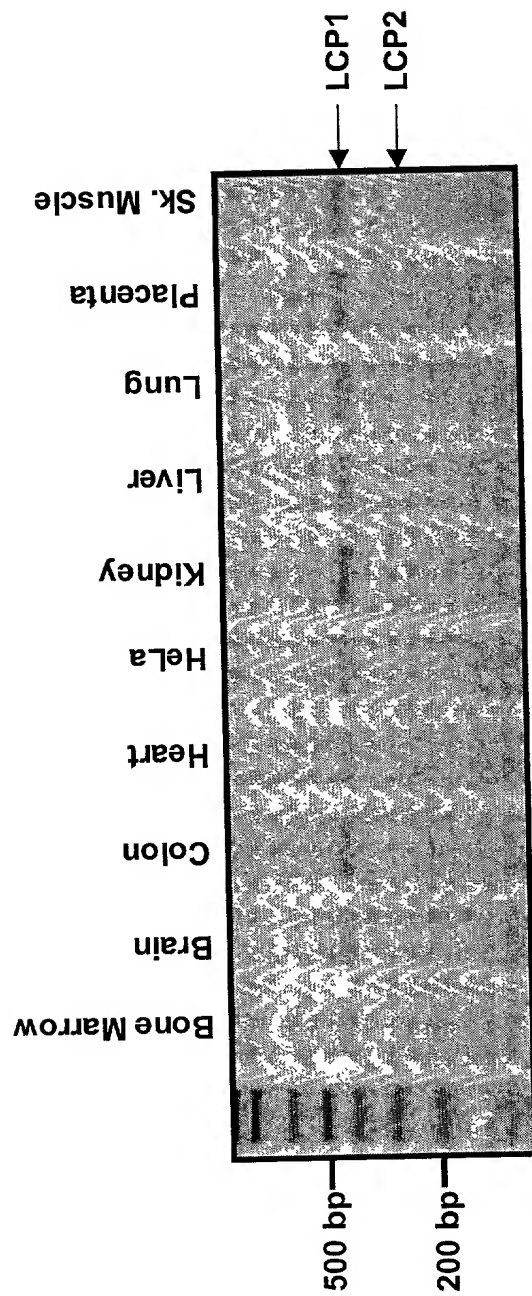


FIG. 5